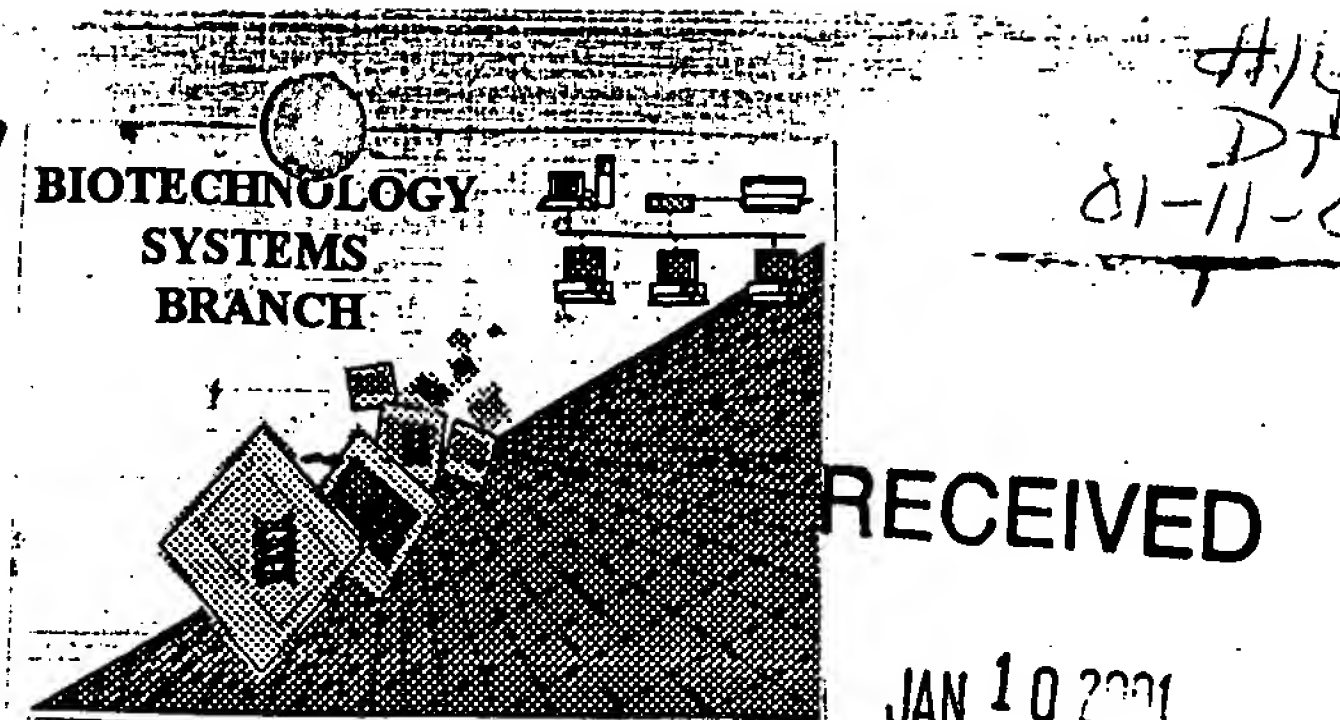


FILE COPY

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,540C

Source: 1643

Date Processed by STIC: 1/2/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/265,540C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- RECEIVED**
JAN 10 2001
TECH CENTER
- 1 Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
 - 2 Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
 - 3 Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
 - 4 Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
 - 5 Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
 - 6 Variable Length
Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
 - 7 PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
 - 8 Skipped Sequences (OLD RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
 - 9 Skipped Sequences (NEW RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
 - 10 Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
 - 11 Use of <213>Organism (NEW RULES)
Sequence(s) are missing this mandatory field or its response.
 - 12 Use of <220>Feature (NEW RULES)
Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
 - 13 PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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1643

JAN 10 2001

RAW SEQUENCE LISTING

DATE: 01/02/2001

PATENT APPLICATION: US/09/265,540C

TIME: 12:53:41

TECH CENTER 1600/2900

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\I265540C.raw

Does Not Comply
Corrected Diskette Needed

pp 2,3,5

3 <110> APPLICANT: Parham, Christi L.
 4 Moore, Kevin W.
 5 Hurgolo, Nicholas J.
 6 Bazan, J. Fernando
 8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 10 <130> FILE REFERENCE: EX0804E
 12 <140> CURRENT APPLICATION NUMBER: 09/265,540C
 13 <141> CURRENT FILING DATE: 1999-03-08
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1381
 21 <212> TYPE: DNA
 22 <213> ORGANISM: primate
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 26 <222> LOCATION: (132)..(1064)
 28 <220> FEATURE:
 29 <221> NAME/KEY: misc_feature
 30 <222> LOCATION: (567)
 31 <223> OTHER INFORMATION: n at position 567; n may be A, C, G, or T;
 32 translated amino acid depends on genetic code
 34 <220> FEATURE:
 35 <221> NAME/KEY: misc_feature
 36 <222> LOCATION: (573)
 37 <223> OTHER INFORMATION: n at position 573; n may be A, C, G, or T;
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 40 <220> FEATURE:
 41 <221> NAME/KEY: misc_feature
 42 <222> LOCATION: (1336)
 43 <223> OTHER INFORMATION: n at position 1336; n may be A, C, G, or T;
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 47 <221> NAME/KEY: misc_feature
 48 <222> LOCATION: (1342)
 49 <223> OTHER INFORMATION: n at position 1342; n may be A, C, G, or T;
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 52 <220> FEATURE:
 53 <221> NAME/KEY: misc_feature
 54 <222> LOCATION: (1369)
 55 <223> OTHER INFORMATION: n at position 1369; n may be A, C, G, or T;
 56 translated amino acid depends on genetic code
 58 <400> SEQUENCE: 1
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 61 agatggtctga gatggacaga atgccttatt ttggaagaa acaatgttct aggtcaaaact 120
 63 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170
 64 Met Glu Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001

TIME: 12:53:41

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\1265540C.raw

	1	5	10	
65				
67	agt ctt ttc atg tgg ttt ttc ttc gca ttg att cca tgt ttg ctc acc			218
68	Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr			
69	15	20	25	
71	gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca			266
72	Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser			
73	30	35	40	45
75	acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc ggc cct gga			314
76	Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly			
77	50	55	60	
79	gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg			362
80	Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu			
81	65	70	75	
83	tac acg agc cac atc tgg atc ccc agc agc ttg tgc tca ctc act gaa			410
84	Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu			
85	80	85	90	
87	ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac			458
88	Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr			
89	95	100	105	
91	aac ctt cgt gtc agc gcc aca ttg ggc tca cag acc tca gcc tga agc			506
92	Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser			
93	110	115	120	125
95	atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct			554
96	Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro			
97	130	135	140	
99	ggg atg gag atc acc aaa aat ggc ttc cac ctg gtt att gag ctg gag			602
100	Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu			
101	145	150	155	
103	gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag			650
104	Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu			
105	160	165	170	
107	cct ggt gcc gag gaa cat gtc aaa atg gtg agc aat ggg ggt att cca			698
108	Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro			
109	175	180	185	
111	gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc			746
112	Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala			
113	190	195	200	205
115	cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca			794
116	Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr			
117	210	215	220	
119	gaa tgt gta gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg			842
120	Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu			
121	225	230	235	
123	ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc			890
124	Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe			
125	240	245	250	
127	gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg			938
128	Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val			
129	255	260	265	

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JAN 10 2001

TECH CENTER 1800/2900

*Please align amino
acids directly under
corresponding codon.*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001

TIME: 12:53:41

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\1265540C.raw

131 gtc ctc cca gac acc ttg aaa ala acc aat tca ccc caa aag tta atc 986
 132 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
 133 270 275 280 285
 135 agc tgc aga agc gag gag gtc gat gcc tgt gcc aag gct gtc atg tct 1034
 136 Ser Cys Arg Arg Gln Gln Val Asp Ala Cys Ala Thr Ala Val Met Ser
 137 290 295 300
 139 cct gag gaa ctc ctc aga gcc tgg atc tca taagttttgcg gaagggccca 1084
 140 Pro Gln Gln Leu Leu Arg Ala Trp Ile Ser
 141 305 310
 143 ggtgaagccg agaacctggc ctgcctgaca tggaaacacat gagaggacaa gtttgtgttc 1144
 145 tgtttttccgc caccgacaaag ggaatgagaga agttaggaaga ggcctgttgc tacaagtcta 1204
 147 gaagcaacca taagagccag ggtgttttgc ckaacagaaac aagtgaactga ggttakraqa 1264
 149 gwtgtgacct ctgacttkfg ggttkscayt tgcwtgqytg agcaagcctg ggaataatga 1324
 151 **W-->** cttcatccct tnggtcnaa gtttttctcat ctgtaatggg ggatncctac aaaactg 1381
 154 <210> SEQ ID NO: 2
 155 <211> LENGTH: 311
 156 <212> TYPE: PRP
 157 <213> ORGANISM: primate
 159 <400> SEQUENCE: 2
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 161 1 5 10 15
 163 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
 164 20 25 30
 166 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
 167 35 40 45
 169 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Gln Thr Val
 170 50 55 60
 172 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Gln Ser Leu Tyr Thr Ser
 173 65 70 75 80
 175 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Gln Gly Pro Gln
 176 85 90 95
 178 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 179 100 105 110
 181 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 182 115 120 125
 184 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 185 130 135 140
W--> 187 Ile **Xaa** Lys **Xaa** Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 188 145 150 155 160
W--> 190 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp **Xaa** Arg Glu Pro Gly Ala
 191 165 170 175
 193 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 194 180 185 190
 196 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 197 195 200 205
W--> 199 Val Lys Ala Ile Gly **Xaa** Tyr Ser Ala Phe Ser Cln Thr Glu Cys Val
 200 210 215 220
W--> 202 **Xaa** Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 203 225 230 235 240

All items on
 Error Summary
 Sheet

RAW SEQUENCE LISTING

PATENT APPLICATION: US/99/265,540C

DATE: 01/03/2001

TIME: 12:53:41

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\1265540C.raw

205 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
 206 245 250 255
 208 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 209 260 265 270
 211 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 212 275 280 285
 214 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Gln Glu
 215 290 295 300
 217 Leu Leu Arg Ala Trp Ile Ser
 218 305 310
 221 <210> SEQ ID NO: 3
 222 <211> LENGTH: 1244
 223 <212> TYPE: DNA
 224 <213> ORGANISM: primate
 225 <220> FEATURE:
 227 <221> NAME/KEY: CDS
 228 <222> LOCATION: (2)..(694)
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 231 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtc cct 49
 232 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
 233 1 5 10 15
 235 tgg ttc ctg tcc tat tgg aat gtt acc att ggg cct cct gag agc atc 97
 236 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 237 20 25 30
 239 tgg gtc aag cag gga gaa gcc tcc ctg atc atc agg ttc tcc tct ccc 145
 240 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
 241 35 40 45
 243 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
 244 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
 245 50 55 60
 247 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
 248 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
 249 65 70 75 80
 251 tcc atc gtc ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289
 252 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
 253 85 90 95
 255 gtg aag gcg cat ctg ttt cgc aca tcc tgc aac acc tct agc ccc ggc 337
 256 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
 257 100 105 110
 259 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385
 260 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
 261 115 120 125
 263 aag ctt caa caa gtc atc ctg atc gcc gtg gga gtc ttt ctg tgg ctg 433
 264 Lys Leu Gln Glu Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
 265 130 135 140
 267 gcc gcc ctg gcc ggg gcc tgt ttc ttc ctg gtg ctg aga tac aaa gcc 481
 268 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
 269 145 150 155 160
 271 ctg gtc aag tac tgg ttt cag tct ccg cca agc atc cca tca caa atc 529

RAW SEQUENCE LISTING

DATE: 01/01/2001

PATENT APPLICATION: US/09/265,540C

TIME: 12:53:41

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\I265540C.raw

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273      165      170      175
275 gaa gaa tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577
276 Glu Glu Tyr Leu Lys Asp Pro Ser Glu Pro Ile Leu Glu Ala Leu Asp
277      180      185      190
279 aag gac acg Lea cca aca gat gat gcc tga gac ttg gtg tct gtt gtt 625
280 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
281      195      200      205
283 gca ttt cca gca aag gaa cca gaa gat gtt ccc caa agc act ttg acc 673
284 Ala Phe Pro Ala Lys Glu Gln Gln Asp Val Pro Gln Ser Thr Leu Thr
285      210      215      220
287 caa aac tct ggt gca gtc tgc tagcctgttg ggtaagggtt ctgagccgaq 724
288 Gln Asn Ser Gly Ala Val Cys
289 225      230
291 gaagctgctg atgtccatgt cagcacttta tggaaatccg tccctccattt tcttgcctcc 784
293 aaaaagccca taagtgcctg taagatgata acgggtctca taaggccgac aagcttatct 844
295 atttttttct tcaactaag agttttctaa tcaatcgcct ttttagaata attctacaga 904
297 tatgtccctg aaagattaa atttctctta aacactaaaa agacalgtaa ttatttctta 964
299 gcaaatgggc gtctggcagc cctctgacac tttttctgta gcagccagga cactgaggtc 1024
301 cctccttgat gaagccctct gggcagacca tctcactatg cccagcctac cccaaagaaq 1081
303 gaatttaagt ggccttctct catatccaaa cacttgctt gaattgtgat tagcctctta 1144
305 aatagtttca caagalttaa gccttttttt ccccaagtt aggaataaaa gactataatt 1204
307 aactttttaa aaaaaaaa aaaaaaaa aaaaaaaa 1244
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 231
312 <212> TYPE: PRP
313 <213> ORGANISM: primate
315 <400> SEQUENCE: 4
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319 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
320      20      25      30
322 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
323      35      40      45
W--> 325 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
326      50      55      60
328 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
329      65      70      75      80
331 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
332      85      90      95
334 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
335      100      105      110
337 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
338      115      120      125
340 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
341      130      135      140
343 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
344      145      150      155      160
346 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001

TIME: 12:53:42

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\I265540C.raw

L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:187 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
 L:187 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
 L:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
 L:187 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
 L:187 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
 L:190 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
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 M:340 Repeated in SeqNo=2
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 L:202 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
 L:244 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
 L:244 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
 L:325 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
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 L:325 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
 L:325 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4